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LGMD gene coding for a calcium dependent protease

The invention relates to the isolated gene coding for a calcium dependent protease belonging to the Calpain family which, when it is mutated, is a cause of a disease called Limb-Girdle Muscular Dystrophy (LGMD).

The term limb-girdle muscular dystrophy (LGMD) was first proposed by Walton and Nattrass (1954) as part of a classification of muscular dystrophies. LGMD is characterised by progressive symmetrical atrophy and weakness of the proximal limb muscles and by elevated serum creatine kinase. Muscle biopsies demonstrate dystrophic lesions and electromyograms show myopathic features. The symptoms usually begin during the first two decades of life and the disease gradually worsens, often resulting in loss of walking ability 10 or 20 years after onset (Bushby, 1994). Yet, the precise nosological definition of LGMD still remains unclear. Consequently, various neuromuscular diseases such as facioscapulohumeral, Becker muscular dystrophies and especially spinal muscular atrophies have been occasionally classified under this diagnosis. For example, a recent study (Arikawa et al., 1991) reported that 17% (out of 41) of LGMD patients showed a dystrophinopathy. These issues highlight the difficulty in undertaking an analysis of the molecular and genetic defect(s) involved in this pathology.

Attempts to identify the genetic basis of this disease go back over 35 years. Morton and Chung (1959) estimated that "the frequency of heterozygous carrier ... is 16 per thousand persons". The same authors also stated that "the segregation analysis gives no evidence on whether these genes in different families are allelic or at different loci". Both autosomal dominant and recessive transmission have been reported, the latter being more common with an estimated prevalence of 10^{-5} (Emery, 1991). The localisation of a gene for a recessive form on chromosome 15 (LGMD2A, MIM 253600; Beckmann et al., 1991) provided the definitive proof that LGMD is a specific genetic entity. Subsequent genetic analyses confirmed this chromosome 15 localisation (Young et al., 1992; Passos-Bueno et al., 1993), the latter group demonstrating genetic heterogeneity of this disease. Although a recent study localised a second mutant

gene to chromosome 2 (LGMD2B, MIM 253601; Bashir et al., 1994), there is evidence that at least one other locus can be involved.

Genetic analyses of the LGMD2 kindreds revealed unexpected findings. First genetic heterogeneity was demonstrated in the highly inbred Indiana Amish community. Second although the Isle of la Réunion families were thought to represent a genetic isolate, at least 6 different disease haplotypes were observed, providing evidence against the hypothesis of a single founder effect (Beckmann et al., 1991) in this inbred population.

The nonspecific nosological definition, the relatively low prevalence and genetic heterogeneity of this disorder limit the number of families which can be used to restrict the genetic boundaries of the LGMD2A interval. Cytogenetic abnormalities, which could have helped to focus on a particular region, have not been reported. Immunogenetic studies of dystrophin-associated proteins (Matsumura et al., 1993) and cytoskeletal or extracellular matrix proteins such as a merosin (Tomé et al., 1994) failed to demonstrate any deficiency. In addition, there is no known specific physiological feature or animal model that could help to identify a candidate gene. Thus, there is no alternative to a positional cloning strategy.

It is established that the LGMD2 chromosomal region is localized on chromosome 15 as 15q15.1 - 15q21.1 region (Fougerousse et al., 1994).

Construction and analysis of a 10-12 Mb YAC contig (Fougerousse et al., 1994) permitted the mapping of 33 polymorphic markers within this interval and to further narrow the LGMD2A region to between D15S514 and D15S222. Furthermore, extensive analysis of linkage disequilibrium suggested a likely position for the gene in the proximal part of the contig.

The invention results from the construction of a partial cosmid map and the screening by cDNA selection (Lovett et al., 1991; Tagle et al., 1993) for muscle-expressed sequences encoded by this interval led to the identification of a number of potential candidate genes. One of these, previously cloned by Sorimachi et al. (1989), encodes a muscle specific protein, nCL1 (novel Calpain Large subunit 1), which belongs to the calpain family (CANP, calcium-activated neutral protease; EC 3.4.22.17), and appeared to be a functional candidate gene for this disease.

Calpains are non-lysosomal intracellular cysteine proteases which require calcium for their catalytic activities (for a review see Croall D.E. et al, 1991). The mammalian calpains include two ubiquitous proteins CANP1 and CANP2 as well as tissue-specific proteins. In addition to the muscle specific nCL1, stomach specific nCL2 and nCL2' proteins have also been described; these are derived from the same gene by alternative splicing. The ubiquitous enzymes consist of heterodimers with distinct large subunits associated with an common small subunit ; the association of tissue-specific large subunits with a small subunit has not yet been demonstrated. The large subunits of calpains can be subdivided into 4 protein domains. Domains I and III, whose functions remain unknown, show no homology with known proteins. Domain I, however, seems important for the regulation of the proteolytic activity. Domain II shows similarity with other cysteine proteases, sharing histidine, cysteine and asparagine residues at its active sites. Domain IV comprises four EF-hand structures which are potential calcium binding sites. In addition, three unique regions with no known homology are present in the muscle-specific nCL1 protein, namely NS, IS1 and IS2, the latter containing a nuclear translocation signal. These regions may be important for the muscle specific function of nCL1.

It is usually accepted that muscular dystrophies are associated with excess or deregulated calpains, and all the known approaches for curing these diseases are the use of antagonists of these proteases ; examples are disclosed in EP 359309 or EP 525420.

The invention results from the finding that, on the opposite to all these hypothesis, the LGMD2 disease is strongly correlated to the defect of a calpain which is expressed in healthy people.

The invention relates to the nucleic acid sequence such as represented in Figure 2 coding for a Ca^{++} dependent protease, or calpain, which is involved in LGMD2 disease, and more precisely LGMD2A. It also relates to a part of this sequence provided it is able to code for a protein having a calcium-dependent protease activity involved in LGMD2, or a sequence derived from one of the above sequences by substitution, deletion or addition of one or more nucleotides provided that said sequence is still coding for said protein, all the nucleic acids yielding a sequence complementary to a sequence as defined above.

The genomic organisation of the human nCL1 gene has been determined by the inventors, and consists of 24 exons and extends over 40 kb as represented in Figure 8, and is also a part of the invention. About 35 kb of this gene have been sequenced. A systematic screening of this gene in LGMD2A families led to the identification of 14 different mutations, establishing that a number of independent mutational events in nCL1 are responsible for LGMD2A. Furthermore, this is the first demonstration of a muscular dystrophy resulting from an enzymatic rather than a structural defect.

In the present specification, CANP3 means the protein which is a Ca^{++} dependent protease, or calpain, and coded by the nCL1 gene on chromosome 15.

The invention relates also to a protein, called CANP3, consisting in the amino acid sequence such as represented in figure 2 and which is involved, when mutated, in the LGMD2 disease.

The cDNA of the gene coding for CANP3, which is coding for the protein, is also represented in Figure 2, and is a part of the invention.

The protein coded by this DNA is CANP3, a calcium-dependent protease belonging to the Calpain family.

Are also included in the present invention the nucleic acid sequences derived from the cDNA of Figure 2 by one or more substitutions, deletions, insertions, or by mutations in 5' or 3' non coding regions or in splice sites, provided that the translated protein has the protease, calcium-dependent activity, and when mutated, induce LGMD2 disease.

The nucleic acid sequence encoding the protein might be DNA or RNA and be complementary to the nucleic acid sequence represented in Figure 2.

The invention also relates to a recombinant vector including a DNA sequence of the invention, under the control of a promoter allowing the expression of the calpain in an appropriate host cell.

A procaryotic or eucaryotic host cell transformed by or transfected with a DNA sequence comprising all or part of the sequence of Figure 2 is a part of the invention.

Such a host cell might be either :

- a cell which is able to secrete the protein and, this recombinant protein might be used as a drug to treat the LGMD2, or

- a packaging cell line transfected by a viral or retroviral vector : the cell lines bearing recombinant vector might be used as a drug for gene therapy of LGMD2.

All the systems used today for gene therapy including adenoviruses and retroviruses and others described for example in « l'ADN médicament », (John Libbey, Eurotext, 1993), and bearing one of the DNA sequence of the invention are included herein by reference.

The examples hereunder and attached figures indicate how the structure of the gene was established, and how relationship between the gene and the LGMD was established.

Legend of the figures :

Figure 1:

A) Genomic organisation of the nCL1 gene

The gene covers a 40 kb region of which 35 were sequenced (Accession number pending). Introns and exons are drawn to scale, the latter being indicated by numbered vertical bars. The first intron is the largest one and remains to be fully sequenced. Position of intragenic microsatellites are indicated by asterisks. Arrows indicate the orientation of Alu (closed) and of Mer2 (greyed) repeat sequences.

B) *EcoRI* restriction map

An *EcoRI* (E) restriction map of this region was established with the help of cosmids from this region. The location of nCL1 gene is indicated as a black bar. The size of the corresponding fragments are indicated and are underlined when determined by sequence analysis.

C) Cosmid map of the nCL1 gene region.

Cosmids were from a cosmid library constructed by subcloning YAC 774G4 (Richard in preparation) and are presented as lines. Dots on lines indicate positive STSs (indicated in boxed rectangles). A minimum of three cosmids cover the entire gene. T3, T7

sub J1
Figure 2: Sequence of the human nCL1 cDNA (B) and the flanking 5' (A) and 3' (C) genomic regions.

A) and C) The polyadenylation signal and putative CAAT, TATAA sites are boxed. Putative Sp1 (position -477 to -472), MEF2 binding sites (-364 to -343) and CArG box (-685 to -672) are in bold. The Alu sequence present in the 5' region is underlined.

C
 B) The corresponding amino acids are shown below the sequence. ^(SEQ ID NO: 6) The coding sequence between the ATG initiation codon and the TGA stop codon is 2466 bp, encoding for a 821 amino acid protein. The adenine in the first methionine codon has been assigned position 1. Locations of introns within the nCL1 gene are indicated by arrowheads. Nucleotides which differ from the previously published ones are indicated by asterisks.

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Figure 3: Alignments of amino acid sequences of the muscle-specific calpains.

The human nCL1 protein is shown on the first line. The 3 muscle-specific sequences (NS, IS1 and IS2) are underlined. ^(SEQ ID NO: 7) The second line corresponds to the rat sequence (Accession no P). The third and fourth lines show the deduced amino acid sequences encoded by pig and bovine Expressed Sequences Tagged (GenBank accession no U05678 and no U07858, respectively). ^(SEQ ID NO: 8 and SEQ ID NO: 9) The amino acids residues which are conserved among all known members of the calpains are in reverse letters. A period indicates that the same amino acid is present in the sequence. Letters refer to the variant amino acid found in the homologous sequence. Position of missense mutations are given as numbers above the mutated amino acid.

Sub G6
Figure 4: Distribution of the mutations along nCL1 protein structure.

A) Positions of the 23 introns are indicated by vertical bars in relation to the corresponding amino acid coordinates.

B) The nCL1 protein is depicted showing the four domains (I, II, III, IV) and the muscle specific sequences (NS, IS1 and IS2). The position of missense mutations within nCL1 domain are indicated by black dots. The effect of nonsense and frameshift mutations are illustrated as truncated lines, representing the extent of protein synthesised. Name of the corresponding families are indicated on the left of the line. The out of frame ORF is given by hatched lines.

Figure 5: Northern blot hybridisation of a nCL1 clone

A mRNA blot (Clontech) containing 2 µg of poly(A)+ RNA from each of eight human tissues was hybridised with a nCL1 genomic clone spanning exons 20 and 21. The latter detects a 3.6 kb mRNA present only in a line corresponding to the skeletal muscle mRNA.

Figure 6: Representative mutations identified by heteroduplex analysis.

Examples of mutation screening by heteroduplex analysis. Pedigree B505 shows the segregation of two different mutations in exon 22.

Figure 7: Homozygous mutations in the nCL1 gene

Detection by sequencing of mutations in exons 2 (a), 8 (b), 13 (c) and 22 (d). Sequences from a healthy control are shown above each mutant sequence. Asterisks indicate the position of the mutated nucleotides. The consequences on codon and amino acid residues are indicated on the left of the figure together with the name of the family.

Figure 8: Structure of nCL1 gene

Figure 8A represents the 5' part of the gene with exon 1. (SEQ ID NO: 1)

Figure 8B represents the part of the gene including exons 2 to 8. (SEQ ID NO: 2)

Figure 8C represents the part of the gene including exon 9. (SEQ ID NO: 3)

Figure 8D represents the part of the gene including exons 10 to 24 including the 3' non transcribed region. (SEQ ID NO: 4)

EXAMPLESEXAMPLE 1Localisation of the nCL1 within the LGMD2A interval

Detailed genetic and physical maps of the LGMD2A region were constructed (Fougerousse et al., 1994), following the primary linkage assignment to 15q (Beckmann et al., 1991). The disease locus was bracketed between the D15S129 and D15S143 markers, defining the cytogenetic boundaries of the LGMD2A region as 15q15.1-15q21.1 (Fougerousse et al., 1994). Construction and analysis of a 10-12 Mb YAC contig (Fougerousse et al., 1994) permitted us to map 33 polymorphic markers within this interval and to further narrow the LGMD2A region to between D15S514 and D15S222.

The nCL1 gene had been localised to chromosome 15 by hybridisation with sorted chromosomes and by Southern hybridisation to DNA from human-mouse cell hybrids (Ohno et al., 1989). cDNA capture using YACs from the LGMD2A interval allowed the identification of thirteen positional candidate genes. nCL1 was one of the two transcripts identified that showed muscle-specific expression as evidenced by northern blot analysis. The localisation was further confirmed by STS (for Sequence Tagged Site) assays. Primers used for the localisation of the nCL1 gene are P94in2, P94in13 and pcr6a3, as shown in Figure 1 and their characteristics being defined in Table 1.

Table 1: PCR primers used for localisation of the nCL1 gene.

Primer name	Primer sequence (5'-3')	Position within the cDNA	Annealing temp (°C)	PCR product size on	
				cDNA	genomic DNA
P94in2	ATGGAGCCAACAGAACTGA C (SEQ ID NO: 10) GTATGACTCGGAAAAGAAG GT (SEQ ID NO: 11)	341-360 428-448	58	108	1758
P94in13	TAAGCAAAAGCAGTCCCA C (SEQ ID NO: 12) TTGCTGTTCTCACTTTCCT G (SEQ ID NO: 13)	1893-1912 1936-1956	58	64	1043
P94-6a3	GTTTCATCTGCTGCTTCGT CTGGTTCAGGCATACATGG T (SEQ ID NO: 15)	2342-2361 2452-2471	56	130	818
P94ex1ter	TTCTTATGTGGACCCTGAG TT (SEQ ID NO: 16) ACGAAGTGGATGGGGAAC	218-239 275-293 (SEQ ID NO: 17)	55	76	76

These primers are designed from different parts of the published human cDNA sequence (Sorimachi et al., 1989), and were used for an STS content screening on DNA from three chromosome 15 somatic cell hybrids and YACs from the LGMD2A contig. The results positioned the gene in a region previously defined as 15q15.1-q21.1 and on 3 YACs (774G4, 926G10, 923G7) localised in this region. The relative positions of STSs along the LGMD2A contig allowed to localise the gene between D15S512 and D15S488, in a candidate region suggested by linkage disequilibrium studies.

The same primers as above were used to screen a cosmid library from YAC 774G4. A group of 5 cosmids was identified (Fig. 1). Experiments with another nCL1 primer pair (P94ex1ter; Table 1) established that these cosmids cover all nCL1 exons except number 1, and that a second group of 4 cosmids contain this

exon (Fig. 1). A minimal set of three overlapping cosmids (2G8-2B11-1F11) covers the entire gene (Figure 1). DNA from these cosmids was used to construct an *EcoRI* restriction map of this region (Figure 1B).

EXAMPLE 2

5 Determination of the nCL1 gene sequence

Most of the sequences were obtained through shotgun sequencing of partial digests of cosmid 1F11 subcloned in M13 and bluescript vectors, and by walking with internal primers. The sequence assembly was made using the XBAP software of the Staden package (Staden) and was in agreement with the
10 restriction map of the cosmids. Sequences of exon 1 and adjacent regions were obtained by sequencing cosmid DNA or PCR products from human genomic DNA. The first intron is still not fully sequenced, but there is evidence that it may be between 10 to 16 kb in length (based on hybridisation of restriction fragments; data not shown). The entire gene, including its 5' and 3' regions, is more than 40
15 kb long, and shown in Figure 8.

a) the cDNA sequence

The used technology allows the implementation of the published human cDNA sequence of nCL1 (Sorimachi 1989). It contains the missing 129 bases corresponding to the N-terminal 43 amino acids (Figure 2). It also differs from it
20 at 12 positions, ^tthree of which occur at third base positions of codons and preserve the encoded amino acid sequence. The other 9 differences lead to changes in amino-acid composition (Figure 2). As these different exons were sequenced repeatedly on at least 10 distinct genomes, we are confident that the sequence of Fig. 2 represents an authentic sequence and does not contain
25 minor polymorphic variants. Furthermore, these modifications increase the local similarity with the rat nCL1 amino acid sequence (Sorimachi), although the overall similarity is still 94 %.

The ATG numbered 1 in Figure 2 is the translation initiation site based on homology with the rat nCL1, and is within a sequence with only 5 nucleotides out
30 of 8 in common with the Kosak consensus sequence (Kosak M, 1984). Putative CCAAT and TATA boxes were observed 590, 324, (CCAAT) and 544 or 33 bp (TATA) upstream of the initiating ATG codon, respectively (Bucher, 1990). A GC-box binding the Sp1 protein (Dyran et al., 1983) was identified at position -477.

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Consensus sequences corresponding to potential muscle-specific regulatory elements were identified (Fig. 2). These include a myocyte-specific enhancer-binding factor 2 (MEF2) binding site (Cserjesi P. 1991), a CArG box (Minty A. 1986) and 6 E-boxes (binding sites for basic Helix-Loop-Helix proteins frequently found in members of MyoD family; Blackwell et Weintraub, 1990). The functional significance of these putative transcription factor binding sites in the regulation of nCL1 gene expression remains to be established.

Two potential AAUAAA polyadenylation signals, were identified 520 and 777 bp downstream of the TGA stop codon. The sequencing of a partial nCL1 cDNA containing a polyA tail, demonstrated that the first AAUAAA is the polyadenylation signal. The latter is embedded in a region well conserved with the rat nCL1 sequence and is followed after 4 bp by a G/T cluster, present in most genes 3' of the polyadenylation site (Birnstiel et al., 1985). The 3'-untranslated region of the nCL1 mRNA is 565 bp long. The predicted length of the cDNA should therefore be approximately 3550 or 3000 bp.

b) Comparison with calpain

The sequence of the human nCL1 gene was compared to those of other calpains thereof (Figure 3). The most telling comparisons are with the homologous rat (Accession no J05121), bovine (Accession no U07858) and porcine (Accession no U05678) sequences. The accession numbers refers to those or international genebanks, such as GeneBank (N.I.H.) or EMBL Database (EMBL, Heidelberg). High local similarities between the human and rat DNA sequences are even observed in the 5' (75%) or in different parts of the 3' untranslated regions (over 60%) (data not shown). The high extent of sequence homology manifested by the human and rat nCL1 gene in their untranslated regions is suggestive of evolutionary pressures on common putative regulatory sequences.

c) Genomic organisation of the nCL1 gene

A comparison of the published nCL1 human cDNA (Sorimachi et al., 1989) with the corresponding genomic sequence led to the identification of 24 exons ranging in length from 12 bp (exon 13) to 309 bp (exon 1), with a mean size of 100 bp (Figure 1). The size of introns ranges from 86 bp to about 10-16 kb for intron 1.

The intron-exon boundaries as shown in Table 2 exhibit close adherence to 5' and 3' splice site consensus sequences (Shapiro and Senapathy, 1987).

Table 2: Sequences at the intron-exon junctions. A score expressing adherence to the consensus was calculated for each site according to Shapiro and Senapathy (1987). Sequences of exons and introns are in upper and lower cases, respectively. Size of exons are given in parenthesis.

splice donor site	score (%)	Intron	score (%)	splice acceptor site	Exon
...CTCCGgigagi...	88.5	<-Intron 1->	99.0	...tttgcacagGAAAT...	Exon 1 (309 bp) ->
...GCTAGgtagga...	83.5	<-Intron 2->	90.0	...ggtcgcctgcagGGGAC...	Exon 2 (70 bp) ->
...TCCAGgigagg...	92	<-Intron 3->	81.5	...acgctctgtagcagTTCTG...	Exon 3 (119 bp) ->
...GCTAAgtaagc...	82	<-Intron 4->	81.5	...atcctctcttaagGCTCC...	Exon 4 (134 bp) ->
...TTGATgtaagi...	87	<-Intron 5->	79.5	...ccatcgggcctcagGATGG...	Exon 5 (169 bp) ->
...CCCGGgigigi...	77.5	<-Intron 6->	91	...ttacigctctacagACAAT...	Exon 6 (144 bp) ->
...ATGAGgtaagc...	94	<-Intron 7->	78.5	...tcigiggttaagGTCCC...	Exon 7 (84 bp) ->
...GATAGgtaggi...	89	<-Intron 8->	91.5	...cattttcccaccagATGGA...	Exon 8 (86 bp) ->
...TTCTGgigagi...	88	<-Intron 9->	92	...ttccaacctctcagGATGT...	Exon 9 (78 bp) ->
...CCCAGgigggga...	80	<-Intron 10->	68.5	...ttcgggggtgcagATACT...	Exon 10 (161 bp) ->
...ACGAGgigigi...	85.5	<-Intron 11->	86	...tgttctctcaagGTTCC...	Exon 11 (170 bp) ->
...AAGAGgtatag...	70	<-Intron 12->	87	...tcccacatctcagATGCA...	Exon 12 (12 bp) ->
...TCTGAgigagi...	76.5	<-Intron 13->	97	...tgtattcctcacagGGAAG...	Exon 13 (209 bp) ->
...CAGTGgigagi...	89	<-Intron 14->	93.5	...cttttctatgcagAAAAA...	Exon 14 (37 bp) ->
...CCAAGgtaggi...	89	<-Intron 15->	87	...ccctctctccagCCCAT...	Exon 15 (18 bp) ->
...CACAGgigtci...	80	<-Intron 16->	88	...ttggtcctccacagCCACA...	Exon 16 (114 bp) ->
...GAGATgigagi...	84	<-Intron 17->	92.5	...cccttctctcagGACAT...	Exon 17 (78 bp) ->
...CAAACgigagi...	83	<-Intron 18->	90	...ctccatccccccagACAAG...	Exon 18 (58 bp) ->
...TGGATgtatcc...	56	<-Intron 19->	88	...cctccctcctccagACAGA...	Exon 19 (65 bp) ->
...GGCAGgigggga...	80	<-Intron 20->	94	...ttctattgccagAAATA...	Exon 20 (69 bp) ->
...CGCAGgigtci...	66	<-Intron 21->	91	...gggtccctccacagGATTC...	Exon 21 (79 bp) ->
					Exon 22 (117 bp) ->

...GTTCAGtaagt...	79	<-Intron 22->	93.5	...gcattctttcacagGAGCT...	Exon 23 (59 bp) ->
...TGGAGGtaaaag...	81	<-Intron 23->	79	...gggaacttctttcagTGGCT...	Exon 24 (27 bp) ->

When the genomic sequence was submitted to GRAIL analysis (Uberbacher et al., 1991), 11 exons were correctly recognised, 4 were not identified, 6 were inadequately defined and 2 were too small to be recognised (data not shown).

5 As already noted, the nCL1 gene has three unique sequence blocks, NS (amino acid residues 1 to 61), IS1 (residues 267 to 329) and IS2 (residues 578 to 653). It is interesting to note that each of these sequences, as well as the nuclear translocation signal inside IS2, are essentially flanked by introns (Fig. 4). The exon-intron organisation of the human nCL1 is similar to that reported for
10 the chicken CANP (the only other large subunit calpain gene whose genomic structure is known; (Emori et al., 1986).

Four microsatellite sequences were identified. Two of them are in the distal part of the first intron: an (AT)₁₄ and an previously identified mixed-pattern microsatellite, S774G4B8, which was demonstrated to be non polymorphic
15 (Fougerousse et al., 1994). A (TA)₇(CA)₄(GA)₁₃ was identified in the second intron and genotyping of 64 CEPH unrelated individuals revealed two alleles (with frequencies of 0.10 and 0.90). The fourth microsatellite is a mixed (CA)_n(TA)_m repeat present in the 9th intron. The latter and the (AT)₁₄ repeat have not been investigated for polymorphism. Fourteen repetitive sequences of
20 the Alu family and one Mer2 repeat were identified in the nCL1 gene (Fig. 1C), which has, thus, on the average one Alu element per 2.5 kb.

Southern blot experiments (Ohno et al., 1989) and STS screening (data not shown) suggest that there is but one copy per genome of this member of the calpain family.

25 EXAMPLE 3

Expression of the nCL1 gene

The pattern of tissue-specificity was investigated by northern blot hybridisation with a genomic subclone probe from cosmid 1F11 spanning exons 20 and 21. There is no evidence for the existence of an alternatively spliced form
30 of nCL1, although this cannot be excluded. A transcript of about 3.4-3.6 kb was

detected in skeletal muscle mRNA (Figure 5). This size therefore favours that the position -544 is the functional TATA box.

Transcription studies suggested that it is an active gene rather than a pseudogene and its muscle-specific pattern of expression is consistent with the phenotype of this disorder (Sorimachi et al., 1989 and Figure 5).

EXAMPLE 4

Mutation screening

nCL1 fulfils both positional and functional criteria to be a candidate gene for LGMD2A. To evaluate its role in the etiology of this disorder, nCL1 was systematically screened in 38 LGMD2 families for the presence of nucleotide changes using a combination of heteroduplex (Keen et al., 1991) and direct sequence analyses.

PCR primers were designed to specifically amplify the exons and splice junctions and also the regions containing the putative CAT, TATA boxes and the polyadenylation signal of the gene as shown in Table 3.

Table 3: PCR primers used for the analysis of the nCL1 gene in LGMD patients.

amplified region	Primer sequences (5'-3')	Size (bp)	Annealing temp. (°C)
promotor	TTCAGTACCTCCCGTTCACC GATGCTTGAGCCAGGAAAAC	(SEQ ID NO: 18) 296	59
exon 1	CTTTCCTTGAAGGTAGCTGTAT GAGGTGCTGAGTGAGAGGAC	(SEQ ID NO: 19) (SEQ ID NO: 20) 438	60
exon 2	ACTCCGTCTCAAAAAAATACCT ATTGTCCCTTTACCTCCTGG	(SEQ ID NO: 21) (SEQ ID NO: 22) 339	57
exon 3	TGGAAGTAGGAGAGTGGGCA GGGTAGATGGGTGGGAAGTT	(SEQ ID NO: 23) (SEQ ID NO: 24) 354	58
exon 4	GAGGAATGTGGAGGAAGGAC TTCCTGTGAGTGAGGTCTCG	(SEQ ID NO: 25) (SEQ ID NO: 26) 292	59
exon 5	GGAACCTCTGTGACCCCAAAT TCCTCAAACAAAACATTTCG	(SEQ ID NO: 27) (SEQ ID NO: 28) 325	56
exon 6	GTTCCCTACATTCTCCATCG GTTATTTCAACCCAGACCCTT	(SEQ ID NO: 29) (SEQ ID NO: 30) 315	57
exon 7	AATGGGTTCTCTGGTTACTGC AGCACGAAAAGCAAAGATAAA	(SEQ ID NO: 31) (SEQ ID NO: 32) 333	56
exon 8	GTAAGAGATTTGCCCCCCCAG TCTGCGGATCATTGGTTTTG	(SEQ ID NO: 33) (SEQ ID NO: 34) 341	58
exon 9	CCTTCCCTTCTTCTGCTTC CTCTCTTCCCCACCCTTACC	(SEQ ID NO: 35) (SEQ ID NO: 36) 173	56
exon 10	CCTCCTCACCTGCTCCCATA TTTTTCGGCTTAGACCCTCC	(SEQ ID NO: 37) (SEQ ID NO: 38) 251	56
exon 11	TGTGGGGAATAGAAATAAATGG CCAGGAGCTCTGTGGGTCA	(SEQ ID NO: 39) (SEQ ID NO: 40) 355	57
exon 12	GGCTCCTCATCCTCATTCA GTGGAGGAGGGTGAGTGTGC	(SEQ ID NO: 41) (SEQ ID NO: 42) 312	61
exon 13	TGTGGCAGGACAGGACGTT	(SEQ ID NO: 43) (SEQ ID NO: 44) 337	60

	14	(SEQ ID NO: 45)	
exon 14	TTCAACCTCTGGAGTGGGCC	(SEQ ID NO: 46)	61
	CACCAGAGCAAACCGTCCAC	(SEQ ID NO: 47)	
exon 15	ACAGCCCAGACTCCCATTCC	(SEQ ID NO: 48)	57
	TTCTCTTCTCCCTTCACCCT	(SEQ ID NO: 49)	
exon 16	ACACACTTCATGCTCTCTACCC	(SEQ ID NO: 50)	56
	CCGCCTATTCCTTTCTCTCT	(SEQ ID NO: 51)	
exon 17	GACAAACTCCTGGGAAGCCT	(SEQ ID NO: 52)	61
	ACCTCTGACCCCTGTGAACC	(SEQ ID NO: 53)	
exon 18	TGTGGATTTGTGTGCTACGC	(SEQ ID NO: 54)	59
	CATAAATAGCACCGACAGGGA	(SEQ ID NO: 55)	
exon 19	GGGATGGAGAAGAGTGAGGA	(SEQ ID NO: 56)	57
	TCCTCACTCTTCTCCATCCC	(SEQ ID NO: 57)	
exons 20-21	ACCCTGTATGTTGCCTTGG	(SEQ ID NO: 58)	61
	GGGGATTTTGTCTGTGCTG	(SEQ ID NO: 59)	
exon 22	ATTCCTGCTCCACCGTCTC	(SEQ ID NO: 60)	57
	CACAGAGTGTCCGAGAGGCA	(SEQ ID NO: 61)	
exons 22-23	GGAGATTATCAGGTGAGATGCC	(SEQ ID NO: 62)	61
	CAGAGTGTCCGAGAGGCAGGG	(SEQ ID NO: 63)	
exon 24	CGTTGACCCCTCCACCTTGA	(SEQ ID NO: 64)	58
	GGGAAAACATGCACCTTCTT	(SEQ ID NO: 65)	
polyadenylation signal	TAGGGGGTAAATGGAGGAG	(SEQ ID NO: 66)	56
	ACTAACTCAGTGGGAATAGGG	(SEQ ID NO: 67)	
	GGAGCTAGGATAGCTCAAT	(SEQ ID NO: 67)	

PCR products made on DNA from blood of specific LGMD2A patients were then subjected either to heteroduplex analysis or to direct sequencing, depending on whether the mutation, based on haplotype analysis, was expected to be homozygous or heterozygous, respectively. It was occasionally necessary to clone the PCR products to precisely identify the mutations (i.e., for microdeletions or insertions and for some heterozygotes). Disease-associated mutations are summarised in Table 4 hereunder and their position along the protein is shown in Fig. 4.

Table 4: nCL1 mutations in LGMD2A families.

Codons and amino acid positions are numbered on the basis of the cDNA sequence starting from ATG.

Exon	Families	Nucleotide position	Nucleotide change	Amino acid position	Amino acid change	Restriction site
2	B519*	328	CGA->TGA	110	Arg->stop	
4	M42	545	CTG->CAG	182	Leu->Gln	
4	M1394; M2888	550	CAA->CA	184	frameshift	
5	M35; M37	701	GGG->GAG	234	Gly->Glu	

15						
6	M32	945	CGG -> CG	315	frameshift	-SmaI
8	M2407*	1061	GIG -> GGG	354	Val-> Gly	
8	M1394	1079	TGG -> TAG	360	Trp->stop	-BstNI, -Eco
11	M2888	1468	CGG -> TGG	490	Arg->Trp	
13	R12*	1715	CGG -> CAG	572	Arg->Gln	-MspI
19	R27	2069-2070	deletion AC	690	frameshift	
21	R14; R17	2230	AGC -> GGC	744	Ser->Gly	-AluI
22	A*: B501*: M32	2306	CGG -> CAG	769	Arg->Gln	
22	B505	2313-2316	deletion AGAC	771-772	frameshift	
22	R14; B505	2362-2363	AG -> TCATCT	788	frameshift	

The first letter of the family code refers to the origin of the population B= Brazil, M= metropolitan France, R = Isle of La Réunion, A= Amish.

Each mutation was confirmed by heteroduplex analysis, by sequencing of both strands in several members of the family or by enzymatic digestion when the mutation resulted in the modification of a restriction site. Segregation analyses of the mutations, performed on DNAs from all available members of the families, confirmed that these sequence variations are on the parental chromosome carrying the LGMD2A mutation. To exclude the possibility that the missense substitutions might be polymorphisms, their presence was systematically tested in a control population: none of these mutations was seen among 120 control chromosomes from the CEPH reference families.

EXAMPLE 5 :

Analysis of families genes, chromosome-15 ascertained families

The initial screening for causative mutations was performed on families, each containing a LGMD gene located on chromosome 15. These included families from the Island of La Réunion (Beckmann et al., 1991), from the Old Order Amish from northern Indiana (Young et al., 1992,) and 2 Brazilian families (Passos Bueno et al., 1993).

a) Reunion Island families

Genealogical studies and geographic isolation of the families from the Isle of La Réunion were suggestive of a single founder effect. Genetic analyses are,

however, inconsistent with this hypothesis as the families present haplotype heterogeneity. At least, six different carrier chromosomes are encountered, (with affected individuals in several families being compound heterozygotes). Distinct mutations corresponding to four of these six haplotypes have been identified thus far.

In family R14, exons 13, 21 and 22 showed evidence for sequence variation upon heteroduplex analysis (Fig. 6). Sequencing of the associated PCR products revealed (i) a polymorphism in exon 13, (ii) a missense mutation (A->G) in exon 21 transforming the Ser⁷⁴⁴ residue to a glycine in the loop of the second EF-hand in domain IV of the protein (Figure 4), and (iii) a frameshift mutation in exon 22. The exon 21 mutation and the polymorphism in exon 13 form an haplotype which is also encountered in family R17. Subcloning of the PCR products was necessary to identify the exon 22 mutation. Sequencing of several clones revealed a replacement of AG by TCATCT (data not shown). This frameshift mutation causes premature termination at nucleotide 2400 where an in frame stop codon occurs (Figure. 4).

The affected individuals in family R12 are homozygous for all markers of the LGMD2A interval (Allamand, submitted). Sequencing of the PCR products of exon 13 revealed a G to A transition at base 1715 of the cDNA resulting in a substitution of glutamine for Arg⁵⁷² (Figure. 7) within domain III, a residue which is highly conserved throughout all known calpains. This mutation, detectable by loss of *MspI* restriction site, is present only in this family and in no other examined LGMD2A families or unrelated controls.

In family R27, heteroduplex analysis followed by sequencing of the PCR products of an affected child revealed a two base pair deletion in exon 19 (Figure. 6 and table 4). One AC out of three is missing at this position of the sequence, producing a stop codon at position 2069 of the cDNA sequence (Figure 4).

b) Amish families

As expected, due to multiple consanguineous links, the examined LGMD2A Northern Indiana Amish patients were homozygous for the haplotype on the chromosome bearing the mutant allele (Allamand, submitted). A (G->A) missense mutation was identified at nucleotide 2306 within exon 22 (Fig. 7). The

Sub G10

Sub G10
resulting codon change is CGG to CAG, transforming Arg⁷⁶⁹ to glutamine. This residue, which is conserved throughout all members of the calpain family in all species, is located in domain IV of the protein within the 3rd EF-hand at the helix-loop junction (ref). This mutation was encountered in a homozygous state in all patients from 12 chromosome 15-linked Amish families, in agreement with the haplotype analysis. We also screened six Southern Indiana Amish LGMD families, for which the chromosome 15 locus was excluded by linkage analyses (Allamand ESHG, submitted, ASHG 94). As expected, this nucleotide change was not present in any of the patients from these families, thus confirming the genetic heterogeneity of this disease in this genetically related isolate.

c) Brazilian families

As a result of consanguineous marriages, two Brazilian families (B501, B519) are homozygous for extended LGMD2A carrier haplotypes (data not shown). Sequencing PCR products from affected individuals of these families demonstrated that family B501 has the same exon 22 mutation found in northern Indiana Amish patients (Figure 7), but embedded in a completely different haplotype. In family B519, the patients carry a C to T transition in exon 2, replacing Arg³²⁸ with a TGA stop codon (Figure 7), thus leading, presumably, to a very truncated protein (Figure 4).

d) Analysis of other LGMD families

Having validated the role of the candidate gene in the chromosome 15 ascertained families, we next examined by heteroduplex analysis LGMD families for which linkage data were not informative. These included one Brazilian (B505) and 13 metropolitan French pedigrees.

Heteroduplex bands were revealed for exons 1, 3, 4, 5, 6, 8, 11, 22 of one or more patients (Figure 6). Of all sequence variants, 10 were identified as possible pathogenic mutations (5 missense, 1 nonsense and 4 frameshift mutations) and 3 as polymorphisms with no change of amino acid of the protein. All causative mutations identified are listed in Table 4 here-above. Identical mutations were uncovered in apparently unrelated families. The mutations shared by families M35 and M37, and M2888 and M1394, respectively, are likely to be the consequence of independent events since they are embedded in different marker haplotypes. In contrast, it is likely that the point mutation in exon

22 of the Amish and in the M32 kindreds corresponds to the same mutational event as both chromosomes share a common four marker haplotype (774G4A1-774G4A10-774G454D-774G4A2) around nCL1 (data not shown), possibly reflecting a common ancestor. The same holds true for the AG to TCATCT substitution mutation encountered in exon 22 in families B505 and R14. The exon 8 (T->G) transversion is present in the two carrier chromosomes of M2407, the only metropolitan family homozygous by haplotype, possibly reflecting an undocumented consanguinity. For some families, no disease-causing mutation has been detected thus far (M40 for example).

In addition to the polymorphism present in exon 13 in families R14 and R17 (position 668) and in the intragenic microsatellites, four additional neutral variations were detected: a (T->C) transition at position 96, abolishing a *DdeI* restriction site in exon 1 in M31; a (C->T) transition in exon 3 (position 495) in M40 and in M37 forming a haplotype with the exon 5 mutation (in the former family, this polymorphism does not cosegregate with the disease); a (T->C) transition in the paternally derived promotor in M42 at position -428, which was also evidenced in healthy controls; and a variable poly(G) in intron 22 close to the splice site in families R20, R11, R19, M35 and M37. The latter is also present in the members of the CEPH families, but is not useful as a genetic marker as the visualisation and interpretation of mononucleotide repeat alleles is difficult.

In total, sixteen independent mutational events representing fourteen different mutations were identified. All mutations cosegregate with the disease in LGMD2A families. The characterised morbid calpain alleles contain nucleotide changes which were not found in alleles from normal individual. The discovery of two nonsense and five frameshift mutations in nCL1 supports the hypothesis that a deficiency of this product causes LGMD2A. All seven mutations result in a premature in-frame stop codon, leading to the production of truncated and presumably inactive proteins (Figure 4). Evidences for the morbidity of the missense mutations come from (1) the relative high incidence of such mutations among LGMD2A patients ; although it is difficult in the absence of functional assays to differentiate between a polymorphism and a morbid mutation, the occurrence of different "missense" mutations in this gene cannot all be

accounted for as rare private polymorphisms: (2) the failure to observe these mutations in control chromosomes; and (3) the occurrence of mutations in evolutionarily conserved residues and/or in regions of documented functional importance. Four of seven missense mutations change an amino acid which is conserved in all known members of the calpain family in all species (Figure 3). Two of the remaining mutations affect less conserved amino acid residues, but are located in important functional domains. The substitution V354G in exon 8 is 4 residues before the asparagine at the active site and S744G in exon 21 is within the loop of the second EF-hand and may impair the calcium-dependent regulation of calpain activity or the interaction with a small subunit (Figure 4). Several missense mutations change a hydrophobic residue to a polar one, or vice versa (Table 4) possibly disrupting higher order structures.

METHODS

Description of the patients

The LGMD2A families analysed were from 4 different geographic origins. They included 3 Brazilian families, 13 interrelated nuclear families from the Isle of la Réunion, 10 French metropolitan families and 12 US Amish families. The majority of these families were previously ascertained to belong to the chromosome 15 group by linkage analysis (Beckmann, 1991; Young, Passos-Bueno et al., 1993). However, some families from metropolitan France as well as one Brazilian family, B505, had non significant lodscores for chromosome 15. Genomic DNA was obtained from peripheral blood lymphocytes.

Sequencing of cosmid c774G4-1F11 and EcoRI restriction map of cosmids.

Cosmid 1F11 (Figure 1C) was subcloned following DNA preparation through Qiagen procedure (Qiagen Inc., USA) and partial digestion with either *Sau3A*, *RsaI* or *AluI*. Size-selected restriction fragments were recovered from low-melting agarose and eventually ligated with M13 or Bluescript (Stratagene, USA) vectors. After electroporation in *E.coli*, recombinant colonies were picked in 100 µl of LB/ampicillin media. PCR reactions were performed on 1 µl of the culture in 10 mM Tris-HCl, pH 9.0, 50 mM KCl, 1.5 mM MgCl₂, 0.1% Triton X-100, 0.01 gelatine, 200µM of each dNTP, 1 U of Taq Polymerase (Amersham) with 100 ng of each vectors primers. Amplification was initiated by 5 min denaturation at 95°C, followed by 30 cycles of 40 sec denaturation at 92°C and 30 sec annealing

at 50°C. PCR products were purified through Microcon devices (Amicon, USA) and sequenced using the dideoxy chain termination method on an ABI sequencer (Applied Biosystems, Foster City, USA). The sequences were analysed and alignments performed using the XBAP software of the Staden package, version 93.9 (Staden, 1982). Gaps between sequence contigs were filled by walking with internal primers. *EcoRI* restriction map of cosmids was performed essentially as described in Sambrook et al. (1989).

Northern Blot analysis

The probes were labelled by random priming with dCTP-($\alpha^{32}\text{P}$). Hybridisation was performed to human multiple tissue northern blots as recommended by the manufacturer (Clontech, USA).

Analysis of PCR products from LGMD2A families

One hundred ng of human DNA were used per PCR under the buffer and cycle conditions described in Fougousse (1994) (annealing temperature shown in Table 3). Heteroduplex analysis (Keene et al., 1991) was performed by electrophoresis of ten μl of PCR products on a 1.5 mm-thick Hydrolink MDE gels (Bioprobe) at 500-600 volt for 12-15 h depending of the fragment length. Migration profile was visualised under UV after ethidium bromide staining.

For sequence analysis, the PCR products were subjected to dye-dideoxy sequencing, after purification through microcon devices (Amicon, USA). When necessary, depending on the nature of the mutations (e.g., frameshift mutation or for some heterozygotes), the PCR products were cloned using the TA cloning kit from Invitrogen (UK). One μl of product was ligated to 25 ng of vector at 12°C overnight. After electroporation into XL1-blue bacteria, several independent clones were analysed by PCR and sequenced as described above.

The invention results from the finding that the nCL1 gene when it is mutated is involved in the etiology of LGMD2A. It is exactly the contrary to what is stated in the litterature, e.g. that the disease is accompanied by the presence of a deregulated calpain. Identification of nCL1 as the defective gene in LGMD2A represents the first example of muscular dystrophy caused by mutation affecting a gene which is not a structural component of muscle tissue, in contrast with previously identified muscular dystrophies such as Duchenne and Becker (Bonilla et al., 1988), severe childhood autosomal recessive (Matsumara et al.,

1992), Fukuyama (Matsumara et al., 1993) and merosin-deficient congenital muscular dystrophies (Tomé et al., 1994).

The understanding of the LGMD2A phenotype needs to take into account the fact that there is no active nCL1 protein in several patients, a loss compatible with the recessive manifestation of this disease. Simple models in which this protease would be involved in the degradation or destabilisation of structural components of the cytoskeleton, extracellular matrix or dystrophin complex can therefore be ruled out. Furthermore, there are no signs of such alterations by immunocytogetic studies on LGMD2 muscle biopsies (Matsumara et al., 1993; Tomé et al., 1994). Likewise, since LGMD2A myofibers are apparently not different from other dystrophic ones, it seems unlikely that this calpain plays a role in myoblast fusion, as proposed for ubiquitous calpains (Wang et al., 1989).

All the data disclosed in these examples confirm that the nCL1 gene is a major gene involved in the disease when mutated.

The fact that morbidity results from the loss of an enzymatic activity raises hopes for novel pharmaco-therapeutic prospects. The availability of transgenic models will be an invaluable tool for these investigations.

The invention is also relative to the use of a nucleic acid or a sequence of nucleic acid of the invention, or to the use of a protein coded by the nucleic acid for the manufacturing of a drug in the prevention or treatment of LGMD2.

The finding that a defective calpain underlies the pathogenesis of LGMD2A may prove useful for the identification of the other loci involved in the LGMDs. Other forms of LGMD may indeed be caused by mutations in genes whose products are the CANP substrates or in genes involved in the regulation of nCL1 expression. Techniques such as the two-hybrid selection system (Fields et al., 1989) could lend themselves to the isolation of the natural protein substrate(s) of this calpain, and thus potentially help to identify other LGMD loci.

The invention also relates to the use of all or a part of the peptidic sequence of the enzyme, or of the enzyme, product of nCL1 gene, for the screening of the ligands of this enzyme, which might be also involved in the etiology and the morbidity of LGMD2.

The ligands which might be involved are for example substrate(s), activators or inhibitors of the enzyme.

The nucleic acids of the invention might also be used in a screening method for the determination of the components which may act on the regulation of the gene expression.

A process of screening using either the enzyme or a host recombinant cell, containing the nCL1 gene and expressing the enzyme, is also a part of the invention.

The pharmacological methods, and the use of nucleic acid and peptidic sequences of the invention are very potent applications.

The methods used for such screenings of ligands or regulatory elements are those described for example for the screening of ligands using cloned receptors.

The identification of mutations in the nCL1 gene provides the means for direct prenatal or presymptomatic diagnosis and carrier detection in families in which both mutations have been identified. Gene-based accurate classification of LGMD2A families should prove useful for the differential diagnosis of this disorder.

The invention relates to a method of detection of a predisposition to LGMD2 in a family or a human being, such method comprising the steps of :

- selecting one or more exons or flanking sequences which are sensitive in said family;
- selecting the primers specific for the or these exons or their flanking sequences, a specific example being the PCR primers of Table 3, or an hybrid thereof,
- amplifying the nucleic acid sequence, the substrate for this amplification being the DNA of the human being to be checked for the predisposition, and
- comparing the amplified sequence to the corresponding sequence derived from Figure 2 or Figure 8.

Table 2 indicates the sequences of the introns-exons junctions, and primers comprising in their structure these junctions are also included in the invention.

All other primers suitable for such RNA or DNA amplification may be used in the method of the invention.

In the same way, any suitable amplification method : PCR (for Polymerase Chain Reaction ®) NASBA ® (for Nucleic acid Sequence Based Amplification), or others might be used.

The methods usually used in the detection of one site mutations, like ASO (Allele specific PCR), LCR, or ARMS (Amplification Refactory Mutation System) may be implemented with the specific primers of the invention.

5 The primers, such as described in Tables 1 and 3, or including junctions of Table 2, or more generally including the flanking sequences of one of the 24 exons are also a part of the invention.

The kit for the detection of a predisposition to LGMD2 by nucleic acid amplification is also in the scope of the invention, such a kit comprises a least PCR primers selected from the group of :

- 10 a) in those described in table 1
b) in those described in table 3
c) those including the introns-exons junctions of Table 2.
d) derived from primers defined in a),b) or c).

15 The nucleic acid sequence of claim 1 to 3 might be inserted in a viral or a retroviral vector, said vector being able to transfect a packaging cell line.

The packaging transfected cell line, might be used as a drug for gene therapy of LGMD2.

The treatment of LGMD2 disease by gene therapy is implemented by a pharmaceutical composition containing a component selected from the group of :

- 20 a) a nucleic acid sequence according to claims 1 to 4,
b) a cell line according to claim 24,
c) an aminoacid sequence according to claims 5 to 9.

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